Amendment to the Specification:

Please amend the specification as follows:

Please replace the pending title with the following title:

METHODS FOR GENERATING CELLULASES

Please replace the paragraph on page 7, lines 28 and 29, with following amended paragraph:

Figure 5 A-C shows an illustration of the full-length DNA (SEQ ID NO:1) and corresponding deduced amino acid sequence of the enzyme (SEQ ID NO:2) of the present invention.

Please replace the paragraph on page 59, line 29 to page 61, line 6, with following amended paragraph:

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequence for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol 48:443, 1970, by the search for similarity method of person & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection. Other algorithms for determining homology or identity include, for example, in addition to a BLAST program (Basic Local Alignment Search Tool at the National Center for Biological Information), ALIGN, AMAS (Analysis of Multiply Aligned Sequences), AMPS (Protein Multiple Sequence Alignment), ASSET (Aligned Segment Statistical Evaluation Tool), BANDS, BESTSCOR, BIOSCAN (Biological Sequence Comparative Analysis Node), BLIMPS (BLocks IMProved Searcher), FASTA, Intervals & Points, BMB, CLUSTAL V, CLUSTAL W,

CONSENSUS, LCONSENSUS, WCONSENSUS, Smith-Waterman algorithm, DARWIN, Las Vegas algorithm, FNAT (Forced Nucleotide Alignment Tool), Framealign, Framesearch, DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis Package), GAP (Global Alignment Program), GENAL, GIBBS, GenQuest, ISSC (Sensitive Sequence Comparison), LALIGN (Local Sequence Alignment), LCP (Local Content Program), MACAW (Multiple Alignment Construction & Analysis Workbench), MAP (Multiple Alignment Program), MBLKP, MBLKN, PIMA (Pattern-Induced Multi-sequence Alignment), SAGA (Sequence Alignment by Genetic Algorithm) and WHAT-IF. Such alignment programs can also be used to screen genome databases to identify polynucleotide sequences having substantially identical sequences. A number of genome databases are available, for example, a substantial portion of the human genome is available as part of the Human Genome Sequencing Project ~~(J. Roach, http://weber.u.Washington.edu/~roach/human_genome_progress2.html) (Gibbs, 1995)~~. At least twenty-one other genomes have already been sequenced, including, for example, *M. genitalium* (Fraser *et al.*, 1995), M. jannaschii (Bult *et al.*, 1996), *H. influenzae* (Fleischmann *et al.*, 1995), *E. coli* (Blattner *et al.*, 1997), and yeast (*S. cerevisiae*) (Mewes *et al.*, 1997), and *D. melanogaster* (Adams *et al.*, 2000). Significant progress has also been made in sequencing the genomes of model organism, such as mouse, *C. elegans*, and *Arabadopsis sp.* Several databases containing genomic information annotated with some functional information are maintained by different organization, and are accessible via the internet~~, for example, http://wwwtigr.org/tdb; http://www.genetics.wisc.edu; http://genome-www.stanford.edu/~ball; http://hiv-web.lanl.gov; http://www.ncbi.nlm.nih.gov; http://www.ebi.ac.uk; http://Pasteur.fr/other/biology; and http://www.genome.wi.mit.edu~~.

Please replace the paragraph on page 61, lines 7 to 28, with following amended paragraph:

One example of a useful algorithm is BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, Nuc. Acids Res. 25:3389-3402, 1977, and Altschul *et al.*, J. Mol. Biol. 215:403-410, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~. This algorithm involves first identifying high scoring sequence

pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectations (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N= -4, and a comparison of both strands.

Please replace the paragraph on page 62, lines 21 to 31, with following amended paragraph:

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet *et al.*, Science 256:1443-1445, 1992; Henikoff and Henikoff, Proteins 17:49-61, 1993). Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National

Biomedical Research Foundation). BLAST programs are accessible through the U.S. National Library of Medicine~~, *e.g.*, at www.ncbi.nlm.nih.gov~~.

Please replace the paragraph on page 67, lines 16 to 29, with following amended paragraph:

Figure 5 is a flow diagram illustrating one embodiment of an identifier process 300 for detecting the presence of a feature in a sequence. The process 300 begins at a start state 302 and then moves to a state 304 wherein a first sequence that is to be checked for features is stored to a memory 115 in the computer system 100. The process 300 then moves to a state 306 wherein a database of sequence features is opened. Such a database would include a list of each feature's attributes along with the name of the feature. For example, a feature name could be "Initiation Codon" and the attribute would be "ATG". Another example would be the feature name "TAATAA Box" and the feature attribute would be "TAATAA". An example of such a database is produced by the University of Wisconsin Genetics Computer Group [[(www.gcg.com)]]. Alternatively, the features may be structural polypeptide motifs such as alpha helices, beta sheets, or functional polypeptide motifs such as enzymatic active sites, helix-turn-helix motifs or other motifs known to those skilled in the art.

Please replace the paragraph on page 73, lines 1 to 19, with following amended paragraph:

A pBluescript II clone containing the DNA (SEQ ID NO:1) encoding the enzyme (SEQ ID NO:2) of the present invention may be obtained from the ATCC, ATCC Deposit No.97245. This pBluescript II clone containing the DNA of the present invention (SEQ ID NO:1) is used to transform *E. coli* XL1 Blue cells and the E. coli XL1 Blue cells are used to inoculate a 5 ml overnight culture of Luria Broth liquid medium. The 5 ml culture was aliquoted into 1 ml aliquots, and each aliquot was used to innoculate 1 liter of 5X LB culture media. Cells were grown overnight in five 2-liter shake flasks at 37° C. Each one liter cell culture pellet was resuspended in 150 ml of 25 mM Tris, pH 8.0 and then spun at 4K rpm for 10 minutes at 4°C. The resulting pellet was resuspended in 5 ml of 25 mM Tris, pH 8.0, and sonicated with a microsonicator tip 10 times at 30 second intervals. The cell debris was spun out in a SS-34 rotor

at 12K rpms for 10 minutes at 4° C. The resulting supernatant was then brought up to 10% ethanol and incubated at 75° C. for 20 minutes. The flocculated proteins were spun out in an SS-34 rotor at 10K rpms for 10 minutes at 4° C. The resultant supernatant was then filtered through a 0.22 micron filter and applied to a weak anion exchange column (Poros, PI). The column was eluted with a 250, 500, 800 mM NaCl step in a 10 mM Tris Base/10 mM Bis Tris Propane buffer at pH 8.0 (anion buffer). The active CMCase fraction came off at the 250 mM step. This fraction was then diluted with the anion buffer to a concentration of 50 mM. It was then applied to a strong anion exchange column (Poros, HQ) and the column was eluted with a 10 column volume gradient from 50 to 250 mM NaCl using anion buffer. A one band fraction of a 35 kD cellulose comes off in this gradient at approximately 150 mM NaCl.

Amendments to the Drawings:

The attached sheet of drawings includes changes to Figure 5C. This corrected sheet places the figure in compliance with the sequence rules.